William B Whitman

List of Publications by Year in descending order

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262 papers

24,966 citations

68 h-index 145 g-index

344 all docs 344 docs citations

times ranked

344

21576 citing authors

#	Article	IF	CITATIONS
1	Prokaryotes: The unseen majority. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 6578-6583.	7.1	3,950
2	Uniting the classification of cultured and uncultured bacteria and archaea using 16S rRNA gene sequences. Nature Reviews Microbiology, 2014, 12, 635-645.	28.6	2,000
3	<i>Metabolic, Phylogenetic, and Ecological Diversity of the Methanogenic Archaea</i> New York Academy of Sciences, 2008, 1125, 171-189.	3.8	998
4	Report of the ad hoc committee for the re-evaluation of the species definition in bacteriology International Journal of Systematic and Evolutionary Microbiology, 2002, 52, 1043-1047.	1.7	971
5	Proposal to reclassify the proteobacterial classes Deltaproteobacteria and Oligoflexia, and the phylum Thermodesulfobacteria into four phyla reflecting major functional capabilities. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5972-6016.	1.7	830
6	The ecological coherence of high bacterial taxonomic ranks. Nature Reviews Microbiology, 2010, 8, 523-529.	28.6	562
7	Quantitative Comparisons of 16S rRNA Gene Sequence Libraries from Environmental Samples. Applied and Environmental Microbiology, 2001, 67, 4374-4376.	3.1	550
8	RNA-Dependent Cysteine Biosynthesis in Archaea. Science, 2005, 307, 1969-1972.	12.6	468
9	Relative impacts of land-use, management intensity and fertilization upon soil microbial community structure in agricultural systems. Soil Biology and Biochemistry, 2008, 40, 2843-2853.	8.8	450
10	RNA-dependent conversion of phosphoserine forms selenocysteine in eukaryotes and archaea. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 18923-18927.	7.1	428
11	Genome sequence of Silicibacter pomeroyi reveals adaptations to the marine environment. Nature, 2004, 432, 910-913.	27.8	415
12	Land-use history has a stronger impact on soil microbial community composition than aboveground vegetation and soil properties. Soil Biology and Biochemistry, 2011, 43, 2184-2193.	8.8	362
13	Measurement of deoxyguanosine/thymidine ratios in complex mixtures by high-performance liquid chromatography for determination of the mole percentage guanine + cytosine of DNA. Journal of Chromatography A, 1989, 479, 297-306.	3.7	320
14	Bacterial Taxa That Limit Sulfur Flux from the Ocean. Science, 2006, 314, 649-652.	12.6	296
15	Phylogenomic analyses of a clade within the roseobacter group suggest taxonomic reassignments of species of the genera Aestuariivita, Citreicella, Loktanella, Nautella, Pelagibaca, Ruegeria, Thalassobius, Thiobacimonas and Tropicibacter, and the proposal of six novel genera. International lournal of Systematic and Evolutionary Microbiology. 2018. 68. 2393-2411.	1.7	293
16	Methanogenesis. Current Biology, 2018, 28, R727-R732.	3.9	267
17	Whole Genome Analyses Suggests that Burkholderia sensu lato Contains Two Additional Novel Genera (Mycetohabitans gen. nov., and Trinickia gen. nov.): Implications for the Evolution of Diazotrophy and Nodulation in the Burkholderiaceae. Genes, 2018, 9, 389.	2.4	252
18	Diversity and Taxonomy of Methanogens. , 1993, , 35-80.		243

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19	Silicibacter pomeroyi sp. nov. and Roseovarius nubinhibens sp. nov., dimethylsulfoniopropionate-demethylating bacteria from marine environments. International Journal of Systematic and Evolutionary Microbiology, 2003, 53, 1261-1269.	1.7	231
20	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. Nature Biotechnology, 2017, 35, 676-683.	17.5	222
21	Complete Genome Sequence of the Genetically Tractable Hydrogenotrophic Methanogen Methanococcus maripaludis. Journal of Bacteriology, 2004, 186, 6956-6969.	2.2	208
22	Molecular and Culture-Based Analyses of Prokaryotic Communities from an Agricultural Soil and the Burrows and Casts of the Earthworm Lumbricus rubellus. Applied and Environmental Microbiology, 2002, 68, 1265-1279.	3.1	206
23	A standardized archaeal taxonomy for the Genome Taxonomy Database. Nature Microbiology, 2021, 6, 946-959.	13.3	198
24	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. PLoS Biology, 2014, 12, e1001920.	5.6	190
25	Nickel-containing factor F430: chromophore of the methylreductase of Methanobacterium Proceedings of the National Academy of Sciences of the United States of America, 1982, 79, 3707-3710.	7.1	178
26	Presence of nickel in Factor F430 from Methanobacteriumbryantii. Biochemical and Biophysical Research Communications, 1980, 92, 1196-1201.	2.1	172
27	Bacterial Catabolism of Dimethylsulfoniopropionate (DMSP). Frontiers in Microbiology, 2011, 2, 172.	3.5	171
28	Linking species richness, biodiversity and ecosystem function in soil systems. Pedobiologia, 2005, 49, 479-497.	1.2	170
29	Isolation and characterization of 22 mesophilic methanococci. Systematic and Applied Microbiology, 1986, 7, 235-240.	2.8	165
30	Genomic Insights into Bacterial DMSP Transformations. Annual Review of Marine Science, 2012, 4, 523-542.	11.6	165
31	Genome-scale analysis of gene function in the hydrogenotrophic methanogenic archaeon $\langle i \rangle$ Methanococcus maripaludis $\langle i \rangle$. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4726-4731.	7.1	149
32	The importance of designating type material for uncultured taxa. Systematic and Applied Microbiology, 2019, 42, 15-21.	2.8	149
33	Identification of uncultured bacteria tightly associated with the intestine of the earthworm Lumbricus rubellus (Lumbricidae; Oligochaeta). Soil Biology and Biochemistry, 2003, 35, 1547-1555.	8.8	144
34	Proposal of the suffix –ota to denote phyla. Addendum to  Proposal to include the rank of phylum in the International Code of Nomenclature of Prokaryotes'. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 967-969.	1.7	136
35	The Methanogenic Bacteria. , 2006, , 165-207.		132
36	Novel pathway for assimilation of dimethylsulphoniopropionate widespread in marine bacteria. Nature, 2011, 473, 208-211.	27.8	126

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37	Transformation of Methanococcus maripaludisand identification of aPstI-like restriction system. FEMS Microbiology Letters, 1994, 121, 309-314.	1.8	125
38	Genome Data Provides High Support for Generic Boundaries in Burkholderia Sensu Lato. Frontiers in Microbiology, 2017, 8, 1154.	3 . 5	122
39	Revised road map to the phylum Firmicutes. , 2009, , 1-13.		118
40	Roadmap for naming uncultivated Archaea and Bacteria. Nature Microbiology, 2020, 5, 987-994.	13.3	115
41	Polycyclovorans algicola gen. nov., sp. nov., an Aromatic-Hydrocarbon-Degrading Marine Bacterium Found Associated with Laboratory Cultures of Marine Phytoplankton. Applied and Environmental Microbiology, 2013, 79, 205-214.	3.1	113
42	Dimethylsulfoniopropionate-Dependent Demethylase (DmdA) from <i>Pelagibacter ubique </i> and <i>Silicibacter pomeroyi </i> Journal of Bacteriology, 2008, 190, 8018-8024.	2.2	111
43	Genome sequences as the type material for taxonomic descriptions of prokaryotes. Systematic and Applied Microbiology, 2015, 38, 217-222.	2.8	107
44	A reconstruction of the metabolism of Methanococcus jannaschii from sequence data. Gene, 1997, 197, GC11-GC26.	2.2	106
45	Differences in the composition and diversity of bacterial communities from agricultural and forest soils. Soil Biology and Biochemistry, 2008, 40, 1294-1305.	8.8	105
46	Soil bacterial community succession during longâ€ŧerm ecosystem development. Molecular Ecology, 2013, 22, 3415-3424.	3.9	105
47	Essential anaplerotic role for the energy-converting hydrogenase Eha in hydrogenotrophic methanogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15473-15478.	7.1	104
48	Genomic Characterization of Methanomicrobiales Reveals Three Classes of Methanogens. PLoS ONE, 2009, 4, e5797.	2.5	103
49	Growth and Plating Efficiency of Methanococci on Agar Media. Applied and Environmental Microbiology, 1983, 46, 220-226.	3.1	101
50	Evolution of Dimethylsulfoniopropionate Metabolism in Marine Phytoplankton and Bacteria. Frontiers in Microbiology, 2017, 8, 637.	3.5	100
51	Desulfonatronum thiodismutans sp. nov., a novel alkaliphilic, sulfate-reducing bacterium capable of lithoautotrophic growth. International Journal of Systematic and Evolutionary Microbiology, 2003, 53, 1327-1332.	1.7	96
52	Spirochaeta americana sp. nov., a new haloalkaliphilic, obligately anaerobic spirochaete isolated from soda Mono Lake in California. International Journal of Systematic and Evolutionary Microbiology, 2003, 53, 815-821.	1.7	95
53	Methanogens: a window into ancient sulfur metabolism. Trends in Microbiology, 2012, 20, 251-258.	7.7	93
54	Solirubrobacter pauli gen. nov., sp. nov., a mesophilic bacterium within the Rubrobacteridae related to common soil clones. International Journal of Systematic and Evolutionary Microbiology, 2003, 53, 485-490.	1.7	92

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55	Genetic Systems for Hydrogenotrophic Methanogens. Methods in Enzymology, 2011, 494, 43-73.	1.0	92
56	Sulfur metabolism in archaea reveals novel processes. Environmental Microbiology, 2012, 14, 2632-2644.	3.8	92
57	Physiology and Biochemistry of the Methane-Producing Archaea. , 2006, , 1050-1079.		85
58	Development of soil microbial communities during tallgrass prairie restoration. Soil Biology and Biochemistry, 2010, 42, 302-312.	8.8	85
59	Proposal to include the rank of phylum in the International Code of Nomenclature of Prokaryotes. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 4284-4287.	1.7	84
60	Modest proposals to expand the type material for naming of prokaryotes. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 2108-2112.	1.7	84
61	Formate-Dependent H ₂ Production by the Mesophilic Methanogen <i>Methanococcus maripaludis</i> . Applied and Environmental Microbiology, 2008, 74, 6584-6590.	3.1	83
62	Bacterial communities in soil mimic patterns of vegetative succession and ecosystem climax but are resilient to change between seasons. Soil Biology and Biochemistry, 2013, 57, 749-757.	8.8	83
63	Microbial community succession and bacterial diversity in soils during 77 000 years of ecosystem development. FEMS Microbiology Ecology, 2008, 64, 129-140.	2.7	82
64	Method for isolation of auxotrophs in the methanogenic archaebacteria: role of the acetyl-CoA pathway of autotrophic CO2 fixation in Methanococcus maripaludis Proceedings of the National Academy of Sciences of the United States of America, 1990, 87, 5598-5602.	7.1	81
65	Polycyclic Aromatic Hydrocarbon Degradation of Phytoplankton-Associated Arenibacter spp. and Description of Arenibacter algicola sp. nov., an Aromatic Hydrocarbon-Degrading Bacterium. Applied and Environmental Microbiology, 2014, 80, 618-628.	3.1	81
66	Meeting report: GenBank microbial genomic taxonomy workshop ($12\hat{a}$ \in "13 May, 2015). Standards in Genomic Sciences, 2016, 11, .	1.5	81
67	Cysteine Is Not the Sulfur Source for Iron-Sulfur Cluster and Methionine Biosynthesis in the Methanogenic Archaeon Methanococcus maripaludis. Journal of Biological Chemistry, 2010, 285, 31923-31929.	3.4	80
68	Facile assay of enzymes unique to the Calvin cycle in intact cells, with special reference to ribulose 1,5-bisphosphate carboxylase. Analytical Biochemistry, 1978, 84, 462-472.	2.4	79
69	Novel chemolithotrophic, thermophilic, anaerobic bacteria Thermolithobacter ferrireducens gen. nov., sp. nov. and Thermolithobacter carboxydivorans sp. nov Extremophiles, 2007, 11, 145-157.	2.3	79
70	Genomic Encyclopedia of Type Strains, Phase I: The one thousand microbial genomes (KMG-I) project. Standards in Genomic Sciences, 2013, 9, 1278-1284.	1.5	79
71	Functionally distinct genes regulated by hydrogen limitation and growth rate in methanogenic Archaea. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 8930-8934.	7.1	78
72	Methanococcus aeolicus sp. nov., a mesophilic, methanogenic archaeon from shallow and deep marine sediments. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 1525-1529.	1.7	77

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73	Genomic Encyclopedia of Bacterial and Archaeal Type Strains, Phase III: the genomes of soil and plant-associated and newly described type strains. Standards in Genomic Sciences, 2015, 10, 26.	1.5	74
74	Porticoccus hydrocarbonoclasticus sp. nov., an Aromatic Hydrocarbon-Degrading Bacterium Identified in Laboratory Cultures of Marine Phytoplankton. Applied and Environmental Microbiology, 2012, 78, 628-637.	3.1	73
75	Transition of microbial communities during the adaption to anaerobic digestion of carrot waste. Bioresource Technology, 2011, 102, 7249-7256.	9.6	72
76	Algiphilus aromaticivorans gen. nov., sp. nov., an aromatic hydrocarbon-degrading bacterium isolated from a culture of the marine dinoflagellate Lingulodinium polyedrum, and proposal of Algiphilaceae fam. nov International Journal of Systematic and Evolutionary Microbiology, 2012, 62, 2743-2749.	1.7	70
77	Quantitative Proteomics of the Archaeon Methanococcus maripaludis Validated by Microarray Analysis and Real Time PCR. Molecular and Cellular Proteomics, 2006, 5, 868-881.	3.8	68
78	Inhibition of D-ribulose 1,5-bisphosphate carboxylase by pyridoxal 5′-phosphate. Biochemical and Biophysical Research Communications, 1976, 71, 1034-1039.	2.1	67
79	Disruption of the Operon Encoding Ehb Hydrogenase Limits Anabolic CO 2 Assimilation in the Archaeon Methanococcus maripaludis. Journal of Bacteriology, 2006, 188, 1373-1380.	2.2	65
80	Road map of the phylum Actinobacteria. , 2012, , 1-28.		65
81	Genetics of Methanococcus: possibilities for functional genomics in Archaea. Molecular Microbiology, 1999, 33, 1-7.	2.5	64
82	Gracilibacter thermotolerans gen. nov., sp. nov., an anaerobic, thermotolerant bacterium from a constructed wetland receiving acid sulfate water. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 2089-2093.	1.7	63
83	Expression Vectors for Methanococcus maripaludis: Overexpression of Acetohydroxyacid Synthase and Î ² -Galactosidase. Genetics, 1999, 152, 1439-1447.	2.9	63
84	Trichococcus patagoniensis sp. nov., a facultative anaerobe that grows at â^3 °C, isolated from penguin guano in Chilean Patagonia. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 2055-2062.	1.7	62
85	Changes in the Soil Bacterial Communities in a Cedar Plantation Invaded by Moso Bamboo. Microbial Ecology, 2014, 67, 421-429.	2.8	62
86	Genome-informed Bradyrhizobium taxonomy: where to from here?. Systematic and Applied Microbiology, 2019, 42, 427-439.	2.8	62
87	Global Responses of <i>Methanococcus maripaludis</i> to Specific Nutrient Limitations and Growth Rate. Journal of Bacteriology, 2008, 190, 2198-2205.	2.2	58
88	Heterologous expression of archaeal selenoprotein genes directed by the SECIS element located in the 3' non-translated region. Molecular Microbiology, 2001, 40, 900-908.	2.5	57
89	Tindallia californiensis sp. nov., a new anaerobic, haloalkaliphilic, spore-forming acetogen isolated from Mono Lake in California. Extremophiles, 2003, 7, 327-334.	2.3	57
90	The Order Methanomicrobiales. , 2006, , 208-230.		57

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91	The Modern Concept of the Procaryote. Journal of Bacteriology, 2009, 191, 2000-2005.	2.2	57
92	Identifying labile DOM components in a coastal ocean through depleted bacterial transcripts and chemical signals. Environmental Microbiology, 2018, 20, 3012-3030.	3.8	56
93	Functional response of the soil microbial community to biochar applications. GCB Bioenergy, 2021, 13, 269-281.	5.6	56
94	Populations of Methanogenic Bacteria in a Georgia Salt Marsh. Applied and Environmental Microbiology, 1988, 54, 1151-1157.	3.1	55
95	Genome Sequence of <i>Thermofilum pendens</i> Reveals an Exceptional Loss of Biosynthetic Pathways without Genome Reduction. Journal of Bacteriology, 2008, 190, 2957-2965.	2.2	53
96	Presence of coenzyme M derivatives in the prosthetic group (coenzyme MF430) of methylcoenzyme M reductase from Methanobacterium thermoautotrophicum. Biochemical and Biophysical Research Communications, 1982, 108, 495-503.	2.1	51
97	Thermococcus thioreducens sp. nov., a novel hyperthermophilic, obligately sulfur-reducing archaeon from a deep-sea hydrothermal vent. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 1612-1618.	1.7	51
98	Proteocatella sphenisci gen. nov., sp. nov., a psychrotolerant, spore-forming anaerobe isolated from penguin guano. International Journal of Systematic and Evolutionary Microbiology, 2009, 59, 2302-2307.	1.7	51
99	Phylum All. Euryarchaeota phy. nov , 2001, , 211-355.		50
100	A Flexible System for Cultivation of <i>Methanococcus </i> li>and Other Formate-Utilizing Methanogens. Archaea, 2017, 2017, 1-12.	2.3	49
101	Biosynthesis of 4-Thiouridine in tRNA in the Methanogenic Archaeon Methanococcus maripaludis*. Journal of Biological Chemistry, 2012, 287, 36683-36692.	3.4	48
102	Engineering the Autotroph <i>Methanococcus maripaludis</i> for Geraniol Production. ACS Synthetic Biology, 2016, 5, 577-581.	3.8	48
103	Abundance of 4Fe–4S motifs in the genomes of methanogens and other prokaryotes. FEMS Microbiology Letters, 2004, 239, 117-123.	1.8	46
104	Metabolism of dimethylsulphoniopropionate by <i><scp>R</scp>uegeria pomeroyi</i> â€ <scp>DSS</scp> â€3. Molecular Microbiology, 2013, 89, 774-791.	2.5	46
105	Role of Amino Acids and Vitamins in Nutrition of Mesophilic <i>Methanococcus</i> spp. Applied and Environmental Microbiology, 1987, 53, 2373-2378.	3.1	46
106	Toward unrestricted use of public genomic data. Science, 2019, 363, 350-352.	12.6	45
107	Anabolic Pathways in Methanogens. , 1993, , 445-472.		44
108	Modification of Rhodospirillum rubrum ribulose bisphosphate carboxylase with pyridoxal phosphate. 1. Identification of a lysyl residue at the active site. Biochemistry, 1978, 17, 1282-1287.	2.5	43

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109	Anaerovirgula multivorans gen. nov., sp. nov., a novel spore-forming, alkaliphilic anaerobe isolated from Owens Lake, California, USA. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 2623-2629.	1.7	43
110	Bacterial Community Diversity in Undisturbed Perhumid Montane Forest Soils in Taiwan. Microbial Ecology, 2010, 59, 369-378.	2.8	43
111	Characterization of Energy-Conserving Hydrogenase B in <i>Methanococcus maripaludis</i> . Journal of Bacteriology, 2010, 192, 4022-4030.	2.2	42
112	Microbial 16S gene-based composition of a sorghum cropped rhizosphere soil under different fertilization managements. Biology and Fertility of Soils, 2015, 51, 661-672.	4.3	41
113	Dialogue on the nomenclature and classification of prokaryotes. Systematic and Applied Microbiology, 2019, 42, 5-14.	2.8	41
114	Biochemical and genetic characterization of an early step in a novel pathway for the biosynthesis of aromatic amino acids and p-aminobenzoic acid in the archaeon Methanococcus maripaludis. Molecular Microbiology, 2006, 62, 1117-1131.	2.5	40
115	Genomic Metrics Applied to Rhizobiales (Hyphomicrobiales): Species Reclassification, Identification of Unauthentic Genomes and False Type Strains. Frontiers in Microbiology, 2021, 12, 614957.	3.5	38
116	Request for revision of the Statutes of the International Committee on Systematics of Prokaryotes. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 584-593.	1.7	38
117	Continuous culture of under defined nutrient conditions. FEMS Microbiology Letters, 2004, 238, 85-91.	1.8	37
118	The Diverse Bacterial Community in Intertidal, Anaerobic Sediments at Sapelo Island, Georgia. Microbial Ecology, 2009, 58, 244-261.	2.8	37
119	The relationship of the whole genome sequence identity to DNA hybridization varies between genera of prokaryotes. Antonie Van Leeuwenhoek, 2015, 107, 241-249.	1.7	37
120	Incorporation of Exogenous Purines and Pyrimidines by <i>Methanococcus voltae</i> and Isolation of Analog-Resistant Mutants. Applied and Environmental Microbiology, 1987, 53, 1822-1826.	3.1	37
121	Detection of methyl salicylate using bi-enzyme electrochemical sensor consisting salicylate hydroxylase and tyrosinase. Biosensors and Bioelectronics, 2016, 85, 603-610.	10.1	36
122	Microbially-Mediated Transformations of Estuarine Dissolved Organic Matter. Frontiers in Marine Science, 2017, 4, .	2.5	36
123	Microbial metagenomes and metatranscriptomes during a coastal phytoplankton bloom. Scientific Data, 2019, 6, 129.	5.3	36
124	Change in Bacterial Community Structure in Response to Disturbance of Natural Hardwood and Secondary Coniferous Forest Soils in Central Taiwan. Microbial Ecology, 2011, 61, 429-437.	2.8	35
125	Changes in structure and function of bacterial communities during coconut leaf vermicomposting. Antonie Van Leeuwenhoek, 2017, 110, 1339-1355.	1.7	35
126	Complete genome sequence of Methanoculleus marisnigri Romesser et al. 1981 type strain JR1. Standards in Genomic Sciences, 2009, 1, 189-196.	1.5	34

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127	A newly-isolated marine methanogen harbors a small cryptic plasmid. Archives of Microbiology, 1985, 142, 259-261.	2.2	33
128	Thermoanaerobacter sulfurigignens sp. nov., an anaerobic thermophilic bacterium that reduces 1â€M thiosulfate to elemental sulfur and tolerates 90â€mM sulfite. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 1429-1434.	1.7	33
129	Changes of soil bacterial communities in bamboo plantations at different elevations. FEMS Microbiology Ecology, 2015, 91, .	2.7	33
130	Transplanting the pathway engineering toolbox to methanogens. Current Opinion in Biotechnology, 2019, 59, 46-54.	6.6	33
131	Two Biosynthetic Pathways for Aromatic Amino Acids in the Archaeon Methanococcus maripaludis. Journal of Bacteriology, 2004, 186, 4940-4950.	2.2	32
132	Arboriscoccus pini gen. nov., sp. nov., an endophyte from a pine tree of the class Alphaproteobacteria, emended description of Geminicoccus roseus, and proposal of Geminicoccaceae fam. nov Systematic and Applied Microbiology, 2018, 41, 94-100.	2.8	32
133	Methanogenic Bacteria., 1985,, 3-84.		32
134	Cloning and phylogenetic analysis of the genes encoding acetohydroxyacid synthase from the archaeon Methanococcus aeolicus. Gene, 1997, 188, 77-84.	2.2	31
135	A call to action for the International Committee on Systematics of Prokaryotes. Trends in Microbiology, 2013, 21, 51-52.	7.7	31
136	Minutes of the International Committee on Systematics of Prokaryotes online discussion on the proposed use of gene sequences as type for naming of prokaryotes, and outcome of vote. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4416-4417.	1.7	31
137	Continuous culture ofMethanococcus maripaludisunder defined nutrient conditions. FEMS Microbiology Letters, 2004, 238, 85-91.	1.8	29
138	Complete genome sequence of Methanocorpusculum labreanum type strain Z. Standards in Genomic Sciences, 2009, 1, 197-203.	1.5	29
139	Cedar and bamboo plantations alter structure and diversity of the soil bacterial community from a hardwood forest in subtropical mountain. Applied Soil Ecology, 2017, 112, 28-33.	4.3	29
140	Draft genome sequences of Bradyrhizobium shewense sp. nov. ERR11T and Bradyrhizobium yuanmingense CCBAU 10071T. Standards in Genomic Sciences, 2017, 12, 74.	1.5	29
141	Reclassification of a Polynucleobacter cosmopolitanus strain isolated from tropical Lake Victoria as Polynucleobacter victoriensis sp. nov International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 5087-5093.	1.7	29
142	Methanococci Use the Diaminopimelate Aminotransferase (DapL) Pathway for Lysine Biosynthesis. Journal of Bacteriology, 2010, 192, 3304-3310.	2.2	28
143	Cysteinyl-tRNA formation: the last puzzle of aminoacyl-tRNA synthesis. FEBS Letters, 1999, 462, 302-306.	2.8	27
144	Soil bacterial communities in native and regenerated perhumid montane forests. Applied Soil Ecology, 2011, 47, 111-118.	4.3	27

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145	Regulatory and Functional Diversity of Methylmercaptopropionate Coenzyme A Ligases from the Dimethylsulfoniopropionate Demethylation Pathway in Ruegeria pomeroyi DSS-3 and Other Proteobacteria. Journal of Bacteriology, 2014, 196, 1275-1285.	2.2	27
146	The Methanogenic Bacteria., 2014,, 123-163.		27
147	Proposal for changes in the International Code of Nomenclature of Prokaryotes: granting priority to Candidatus names. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2174-2175.	1.7	27
148	The complete genome sequence of Staphylothermus marinus reveals differences in sulfur metabolism among heterotrophic Crenarchaeota. BMC Genomics, 2009, 10, 145.	2.8	26
149	Physiology and Biochemistry of the Methane-Producing Archaea. , 2013, , 635-662.		26
150	Draft genome sequence of type strain HBR26T and description of Rhizobium aethiopicum sp. nov Standards in Genomic Sciences, 2017, 12, 14.	1.5	26
151	Raineyella antarctica gen. nov., sp. nov., a psychrotolerant, d-amino-acid-utilizing anaerobe isolated from two geographic locations of the Southern Hemisphere. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 5529-5536.	1.7	26
152	Nonenzymatic acetolactate oxidation to diacetyl by flavin, nicotinamide and quinone coenzymes. Biochimica Et Biophysica Acta - General Subjects, 1995, 1245, 366-370.	2.4	25
153	The anabolic pyruvate oxidoreductase from Methanococcus maripaludis. Archives of Microbiology, 2003, 179, 444-456.	2.2	24
154	The importance of porE and porF in the anabolic pyruvate oxidoreductase of Methanococcus maripaludi s. Archives of Microbiology, 2004, 181, 68-73.	2.2	24
155	The Sac10b Homolog in <i>Methanococcus maripaludis</i> Binds DNA at Specific Sites. Journal of Bacteriology, 2009, 191, 2315-2329.	2.2	24
156	Structures of dimethylsulfoniopropionateâ€dependent demethylase from the marine organism <i>Pelagabacter ubique </i> . Protein Science, 2012, 21, 289-298.	7.6	24
157	Droughtâ€induced variability in dissolved organic matter composition in a marshâ€dominated estuary. Geophysical Research Letters, 2015, 42, 6446-6453.	4.0	24
158	Assembly of Methyl Coenzyme M Reductase in the Methanogenic Archaeon Methanococcus maripaludis. Journal of Bacteriology, 2018, 200, .	2.2	24
159	Modification of Rhodospirillum rubrum ribulose bisphosphate carboxylase with pyridoxal phosphate. 2. Stoichiometry and kinetics of inactivation. Biochemistry, 1978, 17, 1288-1293.	2.5	22
160	Purification and analysis of cobamides of Methanobacterium bryantii by high-performance liquid chromatography. Analytical Biochemistry, 1984, 137, 261-265.	2.4	22
161	Pyruvate oxidation by Methanococcus spp Archives of Microbiology, 1992, 158, 271-275.	2.2	22
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